

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2003, 15:46:23 ; Search time 13.9591 Seconds

(without alignments)  
1225.145 Million cell updates/sec

Title: US-09-988-971-2\_COPY\_94\_176

Perfect score: 446

Sequence: 1 WYEGLSREKAEELLIPGN.....WLYSPRLTFFSLQALVDHY 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	446	100.0	197	4	Q9H135	Q9H135 homo sapien
2	446	100.0	210	4	Q8WY18	Q8WY18 homo sapien
3	446	100.0	261	4	Q9H6Q3	Q9H6Q3 homo sapien
4	412	92.4	179	11	Q9D129	Q9D129 mus musculu
5	412	92.4	259	11	Q9V142	Q9V142 mus musculu
6	403	90.4	259	11	Q8R410	Q8R410 mus musculu
7	247	55.4	502	13	Q9DDK6	Q9DDK6 salmo salar
8	246	55.2	488	13	Q13064	Q13064 xenopus lae
9	243	54.5	151	4	Q9H8T7	Q9H8T7 homo sapien
10	243	54.5	276	4	Q13239	Q13239 homo sapien
11	240	53.8	280	11	Q8Q2X8	Q8Q2X8 mus sapien
12	240	53.8	281	11	Q6O898	Q6O898 mus sapien
13	232.5	52.1	505	4	Q961N1	Q961N1 homo sapien
14	228	51.1	509	6	Q9SM32	Q9SM32 hylobates s
15	227	50.9	509	11	Q91X65	Q91X65 mus musculu
16	220	49.3	509	6	Q95KR7	Q95KR7 salmistr sci

17	214	48.0	496	13	Q93411	Q93411 xenopus lae
18	211	47.3	502	13	Q8G6U9	Q8G6U9 fugu rubrip
19	211	47.3	541	11	Q99PW1	Q99PW1 ratius norv
20	207	46.4	812	15	Q85466	Q85466 y73 sarcoma
21	206	46.2	534	4	Q16248	Q16248 homo sapien
22	206	46.2	534	6	Q95M31	Q95M31 hylobates s
23	206	46.2	537	11	Q62844	Q62844 ratius norv
24	206	46.2	561	4	Q9UJ81	Q9UJ81 homo sapien
25	206	46.2	564	4	Q9UJ82	Q9UJ82 homo sapien
26	205	46.0	517	11	Q63206	Q63206 ratius norv
27	199	44.6	392	15	Q28414	Q28414 feline sarc
28	198.5	44.5	517	5	Q9V9J3	Q9V9J3 diptophila
29	193.5	43.4	503	5	Q8W8U5	Q8W8U5 ephydactia f
30	186	41.7	523	15	Q85477	Q85477 rous sarcom
31	186	41.7	526	15	Q64994	Q64994 rous sarcom
32	186	41.7	535	15	Q93080	Q93080 rous sarcom
33	186	41.7	535	15	Q92957	Q92957 rous sarcom
34	183	41.0	587	15	Q64817	Q64817 avian sarco
35	181	40.6	526	15	Q64993	Q64993 rous sarcom
36	181	40.6	526	15	Q07461	Q07461 rous sarcom
37	179	40.1	545	15	Q86362	Q86362 rous sarcom
38	179	40.1	546	15	Q86363	Q86363 rous sarcom
39	177	39.7	110	15	Q9WK01	Q9WK01 rous sarcom
40	177	39.7	526	15	Q92806	Q92806 rous sarcom
41	177	39.7	542	11	Q93J10	Q93J10 ratius norv
42	176.5	39.6	496	11	Q923M5	Q923M5 mus musculu
43	176.5	39.6	527	5	Q9Y121	Q9Y121 ephydactia f
44	172	38.6	526	15	Q60567	Q60567 rous sarcom
45	168.5	37.8	488	4	Q9H3Y6	Q9H3Y6 homo sapien

## ALIGNMENTS

RESULT 1	
Q9H135	PRELIMINARY; PRT; 197 AA.
AC	Q9H135;
DT	01-MAR-2001 (TREMUREL, 16, Created)
DT	01-MAR-2001 (TREMUREL, 16, Last sequence update)
DT	01-MAR-2002 (TREMUREL, 20, Last annotation update)
DE	DQ977B1.1 (Novel protein tyrosine kinase with Src homology domain 2 (SH2) domain) (Fragment).
GN	DQ977B1.1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	LLOYD D.;
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AL050318; CAB75365.1; -.
DR	HSSP; P06239; ILK.
DR	InterPro; IPR000980; SH2.
DR	Pfam; PF00017; SH2; 1.
DR	PRINTS; PR00401; SH2DOMAIN.
DR	ProDom; P000093; SH2; 1.
DR	SMART; SM00252; SH2; 1.
DR	PROSITE; PS50001; SH2; 1.
FT	NON TER.
FT	NON TER.
SO	SEQUENCE 197 AA; 22124 MW; EF01FE7A855C1F1 CRC64;
Query Match	100.0%; Score 446; DB 4; Length 197;
Best Local Similarity	100.0%; Pred. No. 2.5e-45;
Matches 83; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 WYEGLSREKAEELLIPNPGAFILRESQTRGYSLSVRLSRPASMDRIHYRIHCL 60
Db	30 WYEGLSREKAEELLIPNPGAFILRESQTRGYSLSVRLSRPASMDRIHYRIHCL 89
Qy	61 DNGWLYISPRLTFFSLQALVDHY 83

Db 90 DNGWLYISPRITFPSPALVDHY 112

## RESULT 2

ID 08WY18 PRELIMINARY; PRT; 210 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DE Modulator of antigen receptor signaling, putative splice isoform

DE MARS-V.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RC TISSUE=THYMUS;

RA Loreto M.P., McGlade C.J.;

RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice variant."

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF290986; AAL38198.1; -.

DR InterPro; IPR001452; SH3.

DR Pfam; PF00017; SH2; 1.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR PRODOM; PD000093; SH2; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 1.

DR PROSITE; PS50001; SH2; 1.

DR PROSITE; PS50002; SH3; 1.

KW Receptor.

SO SEQUENCE 210 AA; 23103 MW; BED6220853A472E CRC64;

Query Match 100.0%; Score 446; DB 4; Length 210;  
Best Local Similarity 100.0%; Pred. No. 2,7e-45;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLYEGLSREKAEELLPGNPGAFILRESQTRGYSLSVRLSPASMDIRHYRHCL 60

Db 94 WLYEGLSREKAEELLPGNPGAFILRESQTRGYSLSVRLSPASMDIRHYRHCL 153

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

## RESULT 3

ID 09H603 PRELIMINARY; PRT; 261 AA.

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE CDNA: FLJ21992 f18, clone HE006554 (Src-like adapter protein-2)

DE (Modulator of antigen receptor signaling MARS).

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI\_TaxID=9606;

RC TISSUE=THYMUS;

RA Loreto M.P., McGlade C.J.;

RT "Modulator of Antigen Receptor Signaling (MARS) - putative splice variant."

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

Query Match 100.0%; Score 446; DB 4; Length 261;  
Best Local Similarity 100.0%; Pred. No. 3.4e-45;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WLYEGLSREKAEELLPGNPGAFILRESQTRGYSLSVRLSPASMDIRHYRHCL 60

Db 94 WLYEGLSREKAEELLPGNPGAFILRESQTRGYSLSVRLSPASMDIRHYRHCL 153

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

## RESULT 4

ID 09D129 PRELIMINARY; PRT; 179 AA.

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE A930009E2IRik protein.

DE A930009E2IRik.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RC TISSUE=THYMUS;

RA Loreto M.P., McGlade C.J.;

RT "Modulator of Antigen Receptor Signaling."

RL J. Exp. Med. 194:1263-1276 (2001).

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

QY 61 DNGWLYISPRITFPSPALVDHY 83

Db 154 DNGWLYISPRITFPSPALVDHY 176

RA Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaudo M.F.,  
 RA Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hotman M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Mixture 409,685-690(2001).  
 DR EMBL: AK020837, BAB3223.1, -.  
 DR HSSP: P06239, ILKK.  
 DR MGD: MGI:1925049, A930009E21R1K.  
 DR InterPro: IPR000980, SH2.  
 DR Pfam: PF00017, SH2, 1.  
 DR PRINTS: PR00401, SH2DOMAIN.  
 DR ProDom: PD000093, SH2, 1.  
 DR SMART: SM00252, SH2, 1.  
 DR PROSITE: PS50001, SH2, 1.  
 SQ SEQUENCE 179 AA; 19926 MW; 60477A0CF4003FCD CRC64;

Query Match 92.4%; Score 412; DB 11; Length 179;  
 Best Local Similarity 94.0%; Pred. No. 2,6e-41;  
 Matches 78; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WYEGLSREKAEKELLPPNGGAFILRESQTRGSGSYSLSRPASMWRIRHYRIQL 60  
 Db 13 WYEGLSREKAEKELLPPNGGAFILRESQTRGSGSYSLSRPASMWRIRHYRIQL 72  
 Db 73 DNGWLYISPRITPPSLALVDHY 95

## RESULT 5

Q8V142 PRELIMINARY; PRT; 259 AA.  
 ID Q8V142  
 AC Q8V142;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Modulator of antigen receptor signaling MARS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Loreto M.P., McGlade C.J.;  
 RT "Modulator of Antigen Receptor Signaling (MARS)."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF287467, ALU38196.1, -.  
 DR InterPro: IPR000980, SH2.  
 DR InterPro: IPR001452, SH3.  
 DR Pfam: PF00017, SH2, 1.  
 DR Pfam: PF00018, SH3, 1.  
 DR PRINTS: PR00401, SH2DOMAIN.  
 DR ProDom: PD000093, SH2, 1.  
 DR SMART: SM00252, SH2, 1.  
 DR SMART: SM00326, SH3, 1.  
 DR PROSITE: PS50001, SH2, 1.  
 DR PROSITE: PS50002, SH3, 1.  
 KW Receptor.  
 SQ SEQUENCE 259 AA; 28476 MW; 8270F17CD3FC50A3 CRC64;

Query Match 92.4%; Score 412; DB 11; Length 259;  
 Best Local Similarity 94.0%; Pred. No. 3,9e-41;  
 Matches 78; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WYEGLSREKAEKELLPPNGGAFILRESQTRGSGSYSLSRPASMWRIRHYRIQL 60  
 Db 13 WYEGLSREKAEKELLPPNGGAFILRESQTRGSGSYSLSRPASMWRIRHYRIQL 72  
 Db 73 DNGWLYISPRITPPSLALVDHY 95

Db 93 WYEGLSREKAEKELLPPNGGAFILRESQTRGSGSYSLSRPASMWRIRHYRIQL 152  
 Qy 61 DNGWLYISPRITPPSLALVDHY 83  
 Db 153 DNGWLYISPRITPPSLALVDHY 175

## RESULT 6

Q8R4L0 PRELIMINARY; PRT; 259 AA.  
 ID Q8R4L0  
 AC Q8R4L0;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Src-like adapter protein-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pandey A., Ibarrol N., Kratchmarova I., Fernandez M.,  
 RA Constantinescu S., Ohara O., Sawasdikosol S., Lodish H.F., Mann M.;  
 RT "A novel Src homology 2 domain-containing molecule, Src-like Adapter  
 Protein-2 (SLAP-2), which negatively regulates T cell receptor  
 signaling."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ibarrola N., Mann M., Pandey A.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF44990, AAL86403.1, -.  
 SQ SEQUENCE 259 AA; 28516 MW; 1388E68244152E34 CRC64;

Query Match 90.4%; Score 403; DB 11; Length 259;  
 Best Local Similarity 92.8%; Pred. No. 4,7e-40;  
 Matches 77; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WYEGLSREKAEKELLPPNGGAFILRESQTRGSGSYSLSRPASMWRIRHYRIQL 60  
 Db 93 WYEGLSREKAEKELLPPNGGAFILRESQTRGSGSYSLSRPASMWRIRHYRIQL 152  
 Qy 61 DNGWLYISPRITPPSLALVDHY 83  
 Db 153 DNGWLYISPRITPPSLALVDHY 175

## RESULT 7

Q9DDK6 PRELIMINARY; PRT; 502 AA.  
 ID Q9DDK6  
 AC Q9DDK6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Src-family tyrosine kinase SKC.  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei.  
 OC Proacaanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 OX NCBI\_TaxId=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Horvath I., Male R.;  
 RT "A leukocyte cDNA of Atlantic salmon encoding a Src-family tyrosine  
 kinase."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL: AF321110, AAG38611.1, -.  
 DR HSSP: P08631, IAD5.  
 DR InterPro: IPR000719, Euk\_pkinase.  
 DR InterPro: IPR002290, Ser\_thr\_pkinase.  
 DR InterPro: IPR000980, SH2.  
 DR InterPro: IPR001452, SH3.

Query Match 92.4%; Score 403; DB 11; Length 502;  
 Best Local Similarity 92.8%; Pred. No. 4,7e-40;  
 Matches 77; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

[illegible]

RESULT 8		
ID	NAME	PROT: 468 AA.
AC	013064/	PRELIMINARY;
DT	01-JUL-1997 (TREMBLrel, 04, Created)	
DT	01-JUL-1997 (TREMBLrel, 04, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel, 20, Last annotation update)	
DE	Lyn protein tyrosine kinase.	
GN	LYN.	
OS	Xenopus laevis (African clawed frog).	
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei	
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;	
OC	Xenopodinae; Xenopus.	
CC	NCBI_TaxID=8355;	
CC	[1]	
RP	SEQUENCE FROM N.A.	
RA	Fukami Y., Funahiki K., Sato K.;	
RT	"Nucleotide sequence of Xenopus LYN protein tyrosine kinase."	
RL	Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.	
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.	
DR	EMBL: AB003358; BAA20078.1; -.	
DR	HSSP: P08631; IAD5.	
DR	InterPro: IPR000719; Euk_Pkinase.	
DR	InterPro: IPR000980; SH2.	
DR	InterPro: IPR001452; Tyr_Pkinase.	
DR	InterPro: IPR001245; Tyr_Pkinase.	
DR	Pfam: PF00069; kinase; 1.	
DR	Pfam: PF00017; SH2; 1.	
DR	Pfam: PF00018; SH3; 1.	
DR	PRINTS: PRO0401; SHDDOMAIN.	
DR	PRINTS: PRO0452; SHDDOMAIN.	
DR	PRINTS: PRO0109; TYRKINASE.	
DR	ProDom: PD000001; Euk_Pkinase; 1.	
DR	ProDom: PD000066; SH3; 1.	
DR	ProDom: PD000093; SH2; 1.	
DR	SMART: SM00252; SH2; 1.	
DR	SMART: SM00326; SH3; 1.	
DR	SMART: SM00219; TyrcK; 1.	

```

QY      1  MWELELSAEAEKLLLPNGPGCFPIRSQTRGSGSLSVLSRPAAMRIRHRIHCL 60
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      105  WFKQLIRKDAEQGLLAPGNNPGAFPIRSRERSGYSLSINDCPQGVIRHYRIRTL 164
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY      61  DNGGWLISPIITPSPDALVNY 83
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      165  DNGGYISPIITPSTINEMIGH 187
        |||:::|||||:::|||||:::|||||:::|||||:::|||||:::

```

RESULT 9	
Q9HB17	
ID Q9HB17	PRELIMINARY;
	PRT; 161 AA

01-MAR-2001 [TREMBL:rel\_16, Created]  
DT 01-MAR-2001 [TREMBL:rel\_16, Last sequence update]  
DT 01-JUN-2002 [TREMBL:rel\_21, Last annotation update]  
DT Site-like adapter protein (Fragment).  
DE Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Blachschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.  
RA Jorges, Rd, Schlillabel M.B., Menzel U., Detke M.D., Baumgart C.,  
RA Jahn N., Rosenthal A.;  
RT "Chromosome 8 genomic sequence."  
RL Submitted (Apr-2000) to the EMBL/genbank/DBJ databases.  
RN [2]  
RN SEQUENCE FROM N.A.  
RP Genome Sequencing Center Jena;  
RA Submitted (NOV-2000) to the EMBL/genbank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

DR	EMBL; AF033100; AAC3308.1; 1.
DR	HSSP; P08631; 30CK.
DR	InterPro; IPR000980; SH2.
DR	InterPro; IPR001452; SH3.
DR	Pfam; PF00017; SH2; 1.
DR	Pfam; PF00018; SH3; 1.
DR	PRINTS; PRO0401; SH2DOMAIN.
DR	ProDom; PD000093; SH2; 1.
DR	SMART; SM00252; SH2; 1.
DR	SMART; SM00326; SH3; 1.
DR	PROSITE; PS0001; SH2; 1.
DR	PROSITE; PS0002; SH3; 1.
KW	SH3 domain.
FT	NON TER. 161
SQ	SEQUENCE 161 AA; 18493 MW; FC2855466804EB5B20 CR664;

	Query March	54.5%;	Score 243;	DB 4;	Length 161;
	Best Local Similarity	57.8%;	Pred. No. 3.6e-21;		
	Matches	48;	Conservative	12;	Mismatches 17; Indels 6; Gaps 1.
Qy	1	WLYGSLREAEAEELLPGNGCAFILIRSSORRGSSYSLVPSLSPASMDRIRHRYICL	60		
Db	84	WLFGLRLDRAEELQLQEDPTKVGSEFMIRSESKKGFYSLSLR-----HRYGVHRIIRLL	137		
Qy	61	DNGWLITSPLITFPLSLQALVDHYH	83		
Db	138	PNNWYIISPPLITFQCLDEDLVNHY	160		

RESULT 10

Q13239

PRELIMINARY;

PRT; 276 AA.

AC Q13239; 08QZX8;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Putative SRC-like adapter protein (SLAP) (SRC-like-adapter).  
 GN SLAP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96423054; PubMed=8825655;  
 RA Angrist M., Wells D.E., Chakravarti A., Pandey A.;  
 RT "Chromosomal localization of the mouse Src-1-like adapter protein (Slap)  
 RT gene and its putative human homolog SLA.",  
 RL Genomics 30:623-625 (1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Weijerink P.H.S., Zorn G., Bikker H., Bolhuis P.A., Baas F.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Ohtsuki T., Hatake K., Ikeda M., Tomizuka H., Terui Y., Uwai M.,  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Blechschmidt K., Kalaydjieva L., Goodman R., Gresham D., Baas F.,  
 RA Jonge, Rd., Schilhabel M., Wen G., Menzel U., Dettle M., Baumgart C.,  
 RA Rosenthal A.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BONE MARROW;  
 RA Straube R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; U30473; AAC50357.1; -;  
 DR EMBL; U44403; AAC27652.1; -;  
 DR EMBL; D89077; BA13758.1; -;  
 DR EMBL; AF305872; AAG17933.1; -;  
 DR EMBL; EC007042; AAH07042.1; -;  
 DR HSP; P08631; SHC.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRODOM; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PSS0001; SH2; 1.  
 DR PROSITE; PSS0002; SH3; 1.  
 KW SH3 domain.  
 SQ SEQUENCE 276 AA; 31156 MW; B0FC07D7B2ECA378 CRC64;

Query Match

54.5%; Score 243; DB 4; Length 276;

Best Local Similarity 57.8%; Pred. No. 6, 7e-21;

Matches 48; Conservative 12; Mismatches 17; Indels 6; Gaps 1;

QY 1 WLYEGLSRKAEKELLPGNPGAFILRESQTRGSYSLSVRLSPASMDRIHRYHCL 60

DB 84 WLFEGTGRDAEELQLPDTKGSFMRRESSTKGYSLSR-----HQVHRIIRL 137

QY 61 DNGWYISPRITFPSIQALVDHY 83

DB 138 PNNWYISPRITFQCLEDLVHY 160

RESULT 11

08QZX8

PRELIMINARY;

PRT; 280 AA.

AC 08QZX8;  
 DT 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Src-1-like adapter protein SLAP (Fragment).  
 GN Mus musculus (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ILS, AND ISS;  
 RX MEDLINE=21363810; PubMed=11471062;  
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,  
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;  
 RT "High-throughput sequence identification of gene coding variants  
 RT within alcohol-related QTLs";  
 RL Mamm. Genome 12:657-663 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ILS, AND ISS;  
 RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,  
 RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY079449; AAL87537.1; -;  
 DR EMBL; AY079450; AAL87538.1; -;  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 280 AA; 31549 MW; A05C3BF7FEAD951 CRC4;

Query Match

53.8%; Score 240; DB 11; Length 280;

Best Local Similarity 57.8%; Pred. No. 1, 6e-20;

Matches 48; Conservative 11; Mismatches 18; Indels 6; Gaps 1;

QY 1 WLYEGLSRKAEKELLPGNPGAFILRESQTRGSYSLSVRLSPASMDRIHRYHCL 60

DB 83 WLFEGTGRDAEELQLPDTKGSFMRRESSTKGYSLSR-----HQVHRIIRL 136

QY 61 DNGWYISPRITFPSIQALVDHY 83

DB 137 PNNWYISPRITFQCLEDLVHY 159

RESULT 12

060898

PRELIMINARY;

PRT; 281 AA.

AC 060898;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE SRC-1-like adapter protein.  
 GN SLA OR SLAP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95370243; PubMed=7543898;  
 RA Pandey A., Duan H., Dixit V.M.;  
 RT "Characterization of a novel Src-1-like adapter protein that associates  
 RT with the Eck receptor tyrosine kinase";  
 RL J Biol. Chem. 270:19201-19204 (1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20033985; PubMed=10630289;  
 RA Carrier A., Nguyen C., Victorero G., Granjeaud S., Rocha D.,  
 RA Bernard K., Mazek A., Ferrier P., Malsen M., Naquet P.,

RA Malissen B., Jordan B.;  
 RT "differential gene expression in CD3e- and RAG1-deficient thymuses:  
 RT definition of a set of genes potentially involved in thymocyte  
 RT maturation.";  
 RL Immunogenetics 50:255-270(1999).  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; U29056; AAA82756.1; -  
 DR EMBL; AJ131777; CAB6139.1; -  
 DR HSSP; P16277; 1BLK.  
 DR MGI; MGI:104295; Sla.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW SH3 domain.  
 SQ SEQUENCE 281 AA; 31680 MW; B347921656A74DA1 CRC64;

Query Match 53.8%; Score 240; DB 11; Length 281.  
 Best Local Similarity 57.8%; Pred. No. 1.6e-20;  
 Matches 48; Conservative 11; Mismatches 18; Indels 6; Gaps 1;

QY 1 WLYEGLSRKAEKELLPGNPGAFILRESQTRRGSSLSVRLSPASMDRIHRYHICL 60  
 DB 84 WLFEGIGRDABELLQLPDTKISFMIRESETKGFSLSVR-----HRQVMHRIHRL 137  
 QY 61 DNGWLVSRLTFPSLQALVDHY 83  
 DB 138 PNMWYISPRITFQCLDELVTYH 160

## RESULT 13

ID Q96IN1 PRELIMINARY; PRT; 505 AA.  
 AC Q96IN1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Unknown (protein for MGI:16168).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LYMPH;  
 RA Struhsberg R;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC007371; AA07371.1; -  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1;  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Transferase.  
 SQ SEQUENCE 505 AA; 57706 MW; B5F739BEF8389176 CRC64;

Query Match 52.1%; Score 232.5; DB 4; Length 505;  
 Best Local Similarity 54.2%; Pred. No. 2.5e-19;  
 Matches 45; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

QY 1 WLYEGLSRKAEKELLPGNPGAFILRESQTRRGSSLSVRLSPASMDRIHRYHICL 60  
 DB 124 WFFRSQGRKEARQLAPINKAGSFLIRESETKGAFSLSVK-DVTTOGLIHGYHICRL 182  
 QY 61 DNGWLVSRLTFPSLQALVDHY 83  
 DB 183 DRGGYISPRITFPSLQALVDHY 205

## RESULT 14

ID Q95M32 PRELIMINARY; PRT; 509 AA.  
 AC Q95M32;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Lck protein.  
 GN LCK.  
 OS Hylobates sp. (gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 ON NCBI\_TaxID=9581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Picard C.;  
 RL Thesis (2001), Department of Experimental Oncology Laboratory, U.  
 DR EMBL; AJ320182; CAC44027.1; -  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50010; PROTEIN\_KINASE\_TYR; UNKNOWN\_1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW ATP-binding; Transferase.  
 SQ SEQUENCE 509 AA; 57946 MW; F1BF5C237C8DB7E CRC64;

Query Match 51.1%; Score 228; DB 6; Length 509;  
 Best Local Similarity 54.2%; Pred. No. 8.6e-19;  
 Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

QY 1 WLYEGLSRKAEKELLPGNPGAFILRESQTRRGSSLSVRLSPASMDRIHRYHICL 60  
 DB 127 WFFKNSRKDAERQLAPGNTHSFLIRESETKGAFSLSVK-DVDFDONGEVKHYKIRNL 186  
 QY 61 DNGWLVSRLTFPSLQALVDHY 83  
 DB 187 DNGFYISPRITFPELHLYAHY 209

## RESULT 15

ID Q91X65 PRELIMINARY; PRT; 509 AA.  
 AC Q91X65;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Similar to lymphocyte-specific protein tyrosine kinase.  
 GN LCK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N. A.  
RC TISSUE-SALIVARY GLAND;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC011474; AAH11474.1; -.  
DR MGI; MGI:96756; Lck.  
DR InterPro; IPR000719; Euk\_pkinase.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR ProDom; PD000066; SH3; 1.  
DR ProDom; PD000093; SH2; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; UNKNOWN\_1.  
DR PROSITE; PS00001; SH2; 1.  
DR PROSITE; PS00002; SH3; 1.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 509 AA; 57942 MW; 3513102F49A7FD08 CRC64;

Query Match 50.9%; Score 227; DB 11; Length 509;  
Best Local Similarity 54.2%; Pred. No. 1.1e-18;  
Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;  
QY 1 WLYEGLSRKAEELLIPGPGAPLIRESQTRRGYSLSVRLSRPASMDRIRHYRIHCL 60  
Db 127 WFKNLSSRKDAERQLAPGNTHGSFLIRESESTAGSFSLSVRDPDQNGEVVKKYKIRNL 186  
QY 61 DNGWLYISPRLTFFPSQLALVDHY 83  
Db 187 DNGGFYISPRITFFGLHDLVRYH 209

Search completed: March 24, 2003, 15:50:36  
Job time : 14.9591 secs

